
 WISE (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 27 15:57:41 1999: MasPar time 65.43 Seconds
 620.759 Million cell updates/sec

Tabular output not generated.

Title: >US-08-956-991-2

Description: (1-1910) from US08956991A.pcp

Perfect Score: 13516

Sequence: 1 MWILALSLRFOSFANWFSEDL.....KATGOVTSYICLHLEWTFIC 1910

Scoring table: PAM 150
 Gap 11

Searched: 170751 seqs, 21265608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part 11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 42.028; Variance 241.419; scale 0.174

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
1	13516	100.0	1910	32	W42086	Human Down syndrome-c	0.00e-00
2	11110	82.2	1571	32	W42087	Human Down syndrome-c	0.00e-00
3	2081	15.4	465	33	W55045	Neural adhesion molec	8.94e-14
4	740	5.5	1447	26	R68553	Deleted in colorectal	3.28e-41
5	740	5.5	1728	3	R13144	Deleted in Colorectal	3.28e-41
6	631	4.7	1018	16	R87028	Human contactin.	2.11e-33
7	629	4.7	1018	11	R63759	Human contactin (EMBL	2.92e-33
8	623	4.6	1192	32	W57900	Protein of clone C072	7.83e-33
9	606	4.5	1018	22	W29657	Rat contactin ligand	1.27e-31
10	608	4.5	1028	34	W29657	Homo sapiens D185_1	9.15e-32
11	590	4.4	761	16	R92255	Neural cell adhesion	1.74e-30
12	588	4.4	1304	37	W59994	Human neural cell adh	2.41e-30
13	569	4.2	1911	13	R71725	Human PTP-OB.	5.37e-29
14	569	4.2	1911	24	W27225	Human protein tyrosin	5.37e-29
15	549	4.1	582	16	R92255	Neural cell adhesion	1.40e-27
16	525	3.9	1070	20	W08747	Human colon carcinoma	5.89e-26

17	514	3.8	753	39	W83927	Human T85 protein.	4.10e-25
18	486	3.6	1501	14	R72858	Rat receptor type-pro	3.78e-23
19	394	2.9	400	15	R75203	Tyrosine phosphatase	9.24e-17
20	353	2.6	1251	15	R75201	Tyrosine phosphatase	5.88e-14
21	321	2.4	467	17	R84094	NSK2 receptor with pu	8.56e-12
22	319	2.4	467	34	W62575	Alternatively spliced	1.17e-11
23	319	2.4	475	17	R94982	NSK2 extracellular do	1.17e-11
24	322	2.4	478	16	R92718	Mouse muscle-jocalize	7.34e-12
25	322	2.4	478	16	R92718	Mouse muscle-jocalize	7.34e-12
26	319	2.4	863	34	W62569	Mouse muscle-jocalize	1.17e-11
27	319	2.4	867	34	W62583	Mouse receptor tyrosi	1.17e-11
28	322	2.4	868	16	R92717	Mouse muscle-jocalize	7.34e-12
29	320	2.4	868	25	W25610	Rat muscle-specific k	1.00e-11
30	320	2.4	868	25	W25607	Rat Dmk receptor.	1.00e-11
31	326	2.4	869	25	W25506	Human Dmk receptor.	3.95e-12
32	326	2.4	869	25	W25611	Human muscle-specific	3.95e-12
33	319	2.4	871	34	W62568	Mouse receptor tyrosi	1.17e-11
34	319	2.4	871	17	R84087	NSK2 receptor.	1.17e-11
35	319	2.4	873	17	R84092	NSK2 receptor with al	1.17e-11
36	319	2.4	873	34	W52573	Alternatively spliced	1.17e-11
37	319	2.4	881	17	R84091	NSK2 receptor with al	1.17e-11
38	319	2.4	881	34	W62572	Mouse NSK2 (alternati	1.17e-11
39	320	2.4	1225	30	W52289	Homo sapiens cdo tumo	1.00e-11
40	330	2.4	1242	30	W52287	Rattus norvegicus cdo	2.12e-12
41	317	2.3	863	17	R84088	NSK2 receptor with al	1.59e-11
42	302	2.2	1091	27	W41641	Sequence used in dete	1.50e-10
43	264	2.0	1125	30	W52288	Rattus norvegicus cdo	5.22e-08
44	264	2.0	1139	31	W37779	Rattus norvegicus Cla	5.22e-08
45	262	1.9	2327	3	R15468	Human fibronectin.	7.05e-08

ALIGNMENTS

RESULT	1
ID	W42086 standard; Protein: 1910 AA.
AC	W42086;
DT	28-SEP-1998 (first entry)
DE	Human Down syndrome-cell adhesion molecule DS-CAM1.
KW	DS-CAM1; Down syndrome-cell adhesion molecule; neural cell;
KW	Signal transduction; trisomy 21; mental retardation;
KW	holoprosencephaly; corpus callosum agenesis;
KW	Schizencephaly; diagnosis: assay; human.
OS	Homo sapiens.
FH	Key
FT	Peptide
FT	1..23
FT	/label= Sig-peptide
FT	24..1910
FT	/label= Mat. protein
FT	24..447
FT	/label= :
FT	/note= "immunoglobulin type-C2 domain"
FT	888..1594
FT	/label= FBN
FT	1595..1616
FT	/label= Transmembrane
FT	1617..1910
FT	/label= Cytoplasmic
FT	24..126
FT	/label= Ig1
FT	127..225
FT	/label= Ig2
FT	226..316
FT	/label= Ig3
FT	317..409
FT	/label= Ig4
FT	410..506
FT	/label= Ig5
FT	507..503
FT	/label= Ig6
FT	604..697
FT	/label= Ig7
FT	698..792
FT	Region

FT /label= 198
FT 793..887
FT /label= 199
FT 46..102
FT Disulfide_bond 145..197
FT Disulfide_bond 246..293
FT Disulfide_bond 335..385
FT Disulfide_bond 428..484
FT Disulfide_bond 525..575
FT Disulfide_bond 617..669
FT Disulfide_bond 711..766
FT Disulfide_bond 809..865
FT Disulfide_bond 1307..1359
FT Disulfide_bond 78..80
FT /note= "Asn is N-glycosylated"
FT 106..108
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FT 470..472
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FT 487..489
FT /note= "Asn is N-glycosylated"
FT 658..660
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FT 666..668
FT /note= "Asn is N-glycosylated"
FT 710..712
FT /note= "Asn is N-glycosylated"
FT 748..750
FT /note= "Asn is N-glycosylated"
FT 795..797
FT /note= "Asn is N-glycosylated"
FT 924..926
FT /note= "Asn is N-glycosylated"
FT 1142..1144
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FT 1160..1162
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FT 1250..1252
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FT 1271..1273
FT /note= "Asn is N-glycosylated"
FT 1324..1326
FT /note= "Asn is N-glycosylated"
FT 1341..1343
FT /note= "Asn is N-glycosylated"
FT 1488..1490
FT /note= "Asn is N-glycosylated"
PN W09817795-A1.
PD 30-APR-1998.
PF 23-OCT-1997: U19547.
PR 25-OCT-1996: US-029322.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PI Korenberg JR:
DR WPI: 98-271791/24.
DR N-PSDB: V31981.
PT New isolated Down's Syndrome-cell adhesion molecule - used to
PT development products for detection, diagnosis and therapy of
PT developmental and neurological abnormalities
PS Claim 2: Page 73-78; 109pp; English.
CC This polypeptide comprises Down syndrome-cell adhesion molecule
CC DS-CAM1, a cell surface glycoprotein belonging to a novel subclass
CC of the Ig superfamily with highest homology to neural cell adhesion
CC molecules. Its amino acid sequence was deduced from cDNA clones
CC (see V31981) isolated from a trisomy 21 foetal brain library. A
CC splice variant, DS-CAM2 (see W42087), which is non-membrane bound
CC was also identified. The invention also provides human and murine
CC DS-CAM nucleic acid sequences (see also V31985-88), expression
CC vectors and host cells, transgenic animals, antibodies, antisense
CC oligonucleotides, and primers derived from DS-CAM nucleic acid.
CC DS-CAM polypeptides are associated with developmental and
CC neurological processes. They can be used in e.g. neural prosthetic
CC devices used in entubulation methods of repairing (regenerating)
CC damaged or severed peripheral nerves, and also in bioassays to

CC identify agonists and antagonists. The products can also be
CC used in detection, diagnosis and therapy of developmental and
CC neurological abnormalities such as Down syndrome, mental
CC retardation, holoprosencephaly, agenesis of the corpus callosum,
CC or schizencephaly.
SQ Sequence 1910 AA:

Query Match 100.0%: Score 13516; DB 32; Length 1910;
Best Local Similarity 100.0%: Pred. No. 0.00e+00;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mwlaiaiaifgsianvisedihsalyfnvaslgevfastgtclvpccaagipvtirwyl 60
Qy 1 mwlaiaiaifgsianvisedihsalyfnvaslgevfastgtclvpccaagipvtirwyl 60
Db 61 atgeelydvpgirihvbnlylqifipssitllindnycccaenpskirsqthika 120
Qy 61 atgeelydvpgirihvbnlylqifipssitllindnycccaenpskirsqthika 120
Db 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtvslvgsrflitsta 180
Qy 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtvslvgsrflitsta 180
Db 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtvslvgsrflitsta 180
Qy 121 vlrepytvrvedgktmgnvavfkclipsveaylcvswkdvtvslvgsrflitsta 180
Db 181 lyikdvnedglynrcitrlhytgetrgnsarlfsdpansapsildgfdhrkamaq 240
Qy 181 lyikdvnedglynrcitrlhytgetrgnsarlfsdpansapsildgfdhrkamaq 240
Db 181 lyikdvnedglynrcitrlhytgetrgnsarlfsdpansapsildgfdhrkamaq 240
Qy 181 lyikdvnedglynrcitrlhytgetrgnsarlfsdpansapsildgfdhrkamaq 240
Db 241 rvelpckaiahppeydywlkdmpllsgrfqtvtvglllenirpsdssyscveenryg 300
Qy 241 rvelpckaiahppeydywlkdmpllsgrfqtvtvglllenirpsdssyscveenryg 300
Db 241 rvelpckaiahppeydywlkdmpllsgrfqtvtvglllenirpsdssyscveenryg 300
Qy 241 rvelpckaiahppeydywlkdmpllsgrfqtvtvglllenirpsdssyscveenryg 300
Db 301 takvigrlyvkkpikatisprkksvsgvsiscvtgtedgelwyrngelimgknv 360
Qy 301 takvigrlyvkkpikatisprkksvsgvsiscvtgtedgelwyrngelimgknv 360
Db 361 ritginhenlimdhmvsdsgayqctvrkdklsaqdyqvvedgtpklisafsekvsp 420
Qy 361 ritginhenlimdhmvsdsgayqctvrkdklsaqdyqvvedgtpklisafsekvsp 420
Db 421 aepvslmcnkvkqplrltvtclddprikgsnrisgmitsenrvsnjissgyrdg 480
Qy 421 aepvslmcnkvkqplrltvtclddprikgsnrisgmitsenrvsnjissgyrdg 480
Db 421 aepvslmcnkvkqplrltvtclddprikgsnrisgmitsenrvsnjissgyrdg 480
Qy 421 aepvslmcnkvkqplrltvtclddprikgsnrisgmitsenrvsnjissgyrdg 480
Db 481 vyrciaansagvnylgarivnrgpasirpmkntlaiaqrdtyhcrviyppysikwkn 540
Qy 481 vyrciaansagvnylgarivnrgpasirpmkntlaiaqrdtyhcrviyppysikwkn 540
Db 481 vyrciaansagvnylgarivnrgpasirpmkntlaiaqrdtyhcrviyppysikwkn 540
Qy 481 vyrciaansagvnylgarivnrgpasirpmkntlaiaqrdtyhcrviyppysikwkn 540
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Qy 541 snllpfhrcqvafcnugtlklsdvkqevdeqylcnvlgvpqlstsqsvhvtvkvpfiq 600
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Qy 601 pfeprfsisggrvlipevvvsgdplrltlvqdgprlpslgytclnifstslrsls 660
Db 601 pfeprfsisggrvlipevvvsgdplrltlvqdgprlpslgytclnifstslrsls 660
Qy 601 pfeprfsisggrvlipevvvsgdplrltlvqdgprlpslgytclnifstslrsls 660
Db 661 lmhngnytciaarnaavehqsqilivrppkfvqprddgfygkavilncsaeqpyvt 720
Qy 661 lmhngnytciaarnaavehqsqilivrppkfvqprddgfygkavilncsaeqpyvt 720
Db 661 lmhngnytciaarnaavehqsqilivrppkfvqprddgfygkavilncsaeqpyvt 720
Qy 661 lmhngnytciaarnaavehqsqilivrppkfvqprddgfygkavilncsaeqpyvt 720
Db 721 lvmfkskagvpgpqpialnqriovlslngslilkhvaeedsgytlckvsnadvsksm 780
Qy 721 lvmfkskagvpgpqpialnqriovlslngslilkhvaeedsgytlckvsnadvsksm 780
Db 781 yltvkiipamitsynttlaiaqgqkkmescanabekpilyvwekedilimpemarylvsrk 840
Qy 781 yltvkiipamitsynttlaiaqgqkkmescanabekpilyvwekedilimpemarylvsrk 840
Db 781 yltvkiipamitsynttlaiaqgqkkmescanabekpilyvwekedilimpemarylvsrk 840
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Db 841 evgeevstlqlptvredsgfscainsgygedrglqitvgeppdppeleikvkat 900
Qy 841 evgeevstlqlptvredsgfscainsgygedrglqitvgeppdppeleikvkat 900
Db 841 evgeevstlqlptvredsgfscainsgygedrglqitvgeppdppeleikvkat 900
Qy 841 evgeevstlqlptvredsgfscainsgygedrglqitvgeppdppeleikvkat 900
Db 901 ltlvmgfdgnsptigdydiecknksdswdsagrtkdvspqinsatidihpsstysim 960
Qy 901 ltlvmgfdgnsptigdydiecknksdswdsagrtkdvspqinsatidihpsstysim 960

WIDEOR (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 27 16:17:32 1999; MasPar time 21.88 Seconds
Tabular output not generated. 886.258 Million cell updates/sec

Title: >US-08-956-991-2
Description: (1-1910) from US08956991A.pep
Perfect Score: 13516
Sequence: 1 MWILSLSFOSFANVFSEDL.....KAIGVTSYICLHLEMTFC 1910

Scoring table: PAM 150
Gap 11

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 39.122; Variance 235.804; scale 0.166

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	740	5.5	1447	3	PCT-US94-0 Sequence 2, Applicatio	5.59e-40
2	629	4.7	1018	1	US-08-408-0 Sequence 6, Applicatio	2.28e-32
3	629	4.7	1018	1	US-08-408-0 Sequence 6, Applicatio	2.28e-32
4	629	4.7	1018	1	US-08-714-0 Sequence 6, Applicatio	2.28e-32
5	606	4.5	1018	2	US-08-452-0 Sequence 2, Applicatio	8.48e-31
6	569	4.2	1911	2	US-08-800-0 Sequence 2, Applicatio	2.79e-28
7	569	4.2	1911	3	US-08-348-0 Sequence 5, Applicatio	2.79e-28
8	569	4.2	1911	1	PCT-US94-1 Sequence 5, Applicatio	1.13e-22
9	486	3.6	1501	2	US-08-716-0 Sequence 3, Applicatio	1.13e-22
10	486	3.6	1501	2	US-08-447-0 Sequence 3, Applicatio	1.13e-22
11	379	2.8	946	3	PCT-US95-0 Sequence 13, Applicati	1.51e-15
12	322	2.4	478	3	PCT-US95-0 Sequence 15, Applicati	8.04e-12
13	322	2.4	478	3	PCT-US95-0 Sequence 19, Applicati	8.04e-12
14	322	2.4	868	3	PCT-US95-0 Sequence 21, Applicati	8.04e-12
15	320	2.4	868	2	US-08-374-0 Sequence 1, Applicatio	1.08e-11
16	320	2.4	868	2	US-08-644-0 Sequence 1, Applicatio	1.08e-11
17	326	2.4	869	1	US-08-374-0 Sequence 16, Applicati	4.43e-12
18	326	2.4	869	1	US-08-644-0 Sequence 29, Applicati	4.43e-12
19	282	2.1	2231	2	US-08-153-0 Sequence 16, Applicati	3.01e-09
20	262	1.9	2324	3	PCT-US95-0 Sequence 1, Applicatio	5.59e-08
21	262	1.9	2324	4	US-08-283-0 Sequence 1, Applicatio	5.59e-08
22	262	1.9	2327	4	5455158-1 Patent No. 5455158	5.59e-08
23	262	1.9	2446	2	US-08-551-0 Sequence 2, Applicatio	5.59e-08

24	262	1.9	2446	3	PCT-US93-1	Sequence 2, Applicatio	5.59e-08
25	233	1.7	252	2	US-08-414-	Sequence 57, Applicati	3.67e-06
26	227	1.7	252	2	US-08-414-	Sequence 56, Applicati	8.65e-06
27	235	1.7	287	2	US-08-414-	Sequence 49, Applicati	2.76e-05
28	239	1.7	287	2	US-08-414-	Sequence 48, Applicati	6.50e-06
29	229	1.7	304	2	US-08-414-	Sequence 44, Applicati	6.50e-06
30	229	1.7	308	2	US-08-414-	Sequence 46, Applicati	6.50e-06
31	235	1.7	310	2	US-08-414-	Sequence 45, Applicati	2.76e-06
32	235	1.7	315	2	US-08-414-	Sequence 47, Applicati	2.76e-06
33	229	1.7	325	2	US-08-414-	Sequence 2, Applicatio	6.50e-06
34	229	1.7	325	2	US-08-414-	Sequence 41, Applicati	6.50e-06
35	235	1.7	338	2	US-08-414-	Sequence 42, Applicati	2.76e-06
36	235	1.7	338	2	US-08-414-	Sequence 43, Applicati	2.76e-06
37	234	1.7	419	4	5169835-2	Patent No. 5169835.	3.18e-06
38	232	1.7	549	2	US-08-836-	Sequence 11, Applicati	4.24e-06
39	232	1.7	574	2	US-08-836-	Sequence 21, Applicati	4.24e-06
40	227	1.7	642	1	US-08-217-	Sequence 1, Applicatio	8.65e-06
41	227	1.7	734	2	US-08-389-	Sequence 17, Applicati	8.65e-06
42	234	1.7	828	1	US-08-261-	Sequence 2, Applicatio	3.18e-06
43	222	1.6	338	2	US-08-414-	Sequence 60, Applicati	1.76e-05
44	223	1.6	424	4	5169835-6	Patent No. 5169835.	1.53e-05
45	219	1.6	999	1	US-08-252-	Sequence 2, Applicatio	2.69e-05

ALIGNMENT:

RESULT 1
ID PCT-US94-05277-2 STANDARD: PRT: 1447 AA.
XX
AC xxxxxx
DT
DE Sequence 2, Application PC/TUS9405277
XX
CC Sequence 2, Application PC/TUS9405277
CC GENERAL INFORMATION:
CC APPLICANT: Bruskin, Arthur
CC APPLICANT: Jarosz, David E.
CC APPLICANT: Johnson, Karen
CC APPLICANT: Kinzel, Kenneth W.
CC APPLICANT: Vogelst. in, Bert
CC APPLICANT: Zabrecky, James R.
CC TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
CC NUMBER OF SEQUENCES: 2
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Banner, Birch, McKie & Beckett
CC STREET: 1001 G Street, N.W.
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: USA
CC ZIP: 20001
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/05277
CC FILING DATE:
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kagan, Sarah A.
CC REGISTRATION NUMBER: 32,141
CC REFERENCE/DOCKET NUMBER: 01107.42709
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202.508.9100
CC TELEFAX: 202.508.9299
CC TELEX: 197430 BBMB UT
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1447 amino acids
CC TYPE: amino acid

CC TOPOLOGY: linear
CC MOLECULE TYPE: Protein
CC SEQUENCE 1447 AA: 158455 MW: 11668854 CN:
Query Match 5.5%: Score 740: DB 3: Length 1447:
Best Local Similarity 29.44: Pred. No. 5.56e-40:
Matches 226: Conservative 179: Mismatches 295: Indels 70: Gaps 53:
DB 72 IKWKDGIHLALGMDERKQOLNSGSLLIQNLHSHRHHKPDGLGYCEASLGSGSIISRT 131
135 IKWKNS-NL-LPENHROVAFENNGLT-L-K-LSDVQKEVEGYTCNV-LVQPOLSTSSOS 588
DB 132 AKVAVAGPLRLSOTESTAF-MGDTVLKCEVIGEMPM-TIMOKKQDOLTFIPDGRV 189
589 VHVTVKVP-PEIQPE-FPRFSIQARVFIPCVVSGDLPITITWQKGRPIPSLGITID 646
DB 190 VLVLSGALQIRLOPGDIGIRCSARNPASSRTGNEAEVRLSDPGLHROLTYLQRPSTV 249
647 NIDTSSLRISNLHMGNTCTIARNDAAL-VEHOSOL-IVRVP--PK--FVVO-PRDQ 699
DB 250 VAIEGKDAVLECCVGYPPPSFTN-L-RGEEVIQLR--S-K-KYSLGSSNLLISNVTDD 303
700 DGIYKAVILNCSAGEYVPVITWKFSGAGVPOFOPIALNGRIQVLSNGLLIKHYVEE 759
DB 304 DSGMTCTVYTK-NENISASALTYLVPPMFLNHPNLVAVESMDIEFFECTVSG-KPVP 361
760 DSGYLLCKVSDVADGADSKSWLYTKIPAMITSPNTTITOGOKKEMSCITANGELPI-1 818
DB 362 VNMKNGDVIPS-D-YF-QI--VGG--SNLRILGVYKSDGFGYQCAENEAQNTSA 413
819 VRMEKEDILINPEMARVLYSTKEGEEVISTLOJLPIVREDSGFGFCHAINSXYGEGII 878
DB 414 QLIYKPAIPSSSVLPSPADVPVLYVSSRFVRLSWRPAKGNIOITFYFREDNR 473
879 QLIQVEP--PDP--PEI-EIKDV--KARITTLRMWGMFGDGNSPITIGYDECKNKSDSW 929
DB 474 ERLVLTQPGS-IQ-LTVGNLKPAMTYFRVAVANEMGPGSSQPIKVAIQPELQVGPV 531
930 DSAORTKQVSPQLNSATIIDIHPSSTYSTRMYAKNRIGKSEPSNELTITAD-EAAPGPP 988
DB 532 ENLQAVSTSPSILITWEPRA-Y-ANGPVQGRLECTEVSTGKE-Q-NI-EVD--GLS-- 582
989 QEVHLEPTSSQSTRTWMAKPKHLONGIIRGOIGQREYSTGNGFQENIISVDTSQSEV 1048
DB 583 YKLECLKFTEYSLEFLVYNRGPGVSTDITVTVLSVPSAPPNQVSLVENSRSIKVS 642
1049 YTLDMLNKFTQYGLVVOACNRAGTGPSSQOEIITTTLEDVPSYPPENVOAIATSESSIS 1108
DB 643 WLPPSGTONGFITGKIRHKKTRGEM-ETLE-PNMLWYL-FGLGKSGSYSFQVSAM 699
1109 WSTLSKEALNGILOGFRVIYANANLMDGELGKNTITTOPSLDGLGLEYKTNYSIOVLAF 1168
DB 700 TVNGTGPPSNMYTAEPTENDIDESOVDPQSSLHVRPOTNCII-MSWTPPLNPIVVRGY 758
1169 TRAGDQVRSE-QIFTRKE-D---VPCPPAGVKAASASVFWSPMLPKLNGIIRKY 1222
DB 759 IIGYGVGSYATVAV-DSK-QRY-YSTERLESSSHYVLSLKAFNNAGEG 805
QY 1223 TV-F-CSHPYPIVISEFEASPDSPSTIRIPNLISRNQISVWVAVTSAGRG 1270

CC APPLICANT: Reid, Robert A.
CC APPLICANT: Hempel, John J.
CC TITLE OF INVENTION: Human Cell Adhesion Molecule and Nucleic
CC TITLE OF INVENTION: Acid Sequences
CC NUMBER OF SEQUENCES: 6
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Richard J. Rodrick, Becton Dickinson
CC ADDRESSEE: and Company
CC STREET: One Becton Drive
CC CITY: Franklin Lakes
CC STATE: NJ
CC COUNTRY: USA
CC ZIP: 07417
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent, Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/408,093
CC FILING DATE: 21-MAR-1995
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/08/040,741
CC FILING DATE: 26 MAR 1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fugit, Donna R. 32,135
CC REGISTRATION NUMBER: 32,135
CC REFERENCE/DOCKET NUMBER: P-2630
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1018 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: Homo sapiens
CC NAME/KEY: Disulfide-bond
CC LOCATION: 45..94
CC FEATURE:
CC NAME/KEY: Disulfide-bond
CC LOCATION: 138..191
CC FEATURE:
CC NAME/KEY: Disulfide-bond
CC LOCATION: 243..290
CC FEATURE:
CC NAME/KEY: Disulfide-bond
CC LOCATION: 432..471
CC FEATURE:
CC NAME/KEY: Disulfide-bond
CC LOCATION: 416..464
CC FEATURE:
CC NAME/KEY: Disulfide-bond
CC LOCATION: 506..563
CC FEATURE:
CC NAME/KEY: Domain
CC LOCATION: 604..657
CC OTHER INFORMATION: /label= FLR
CC OTHER INFORMATION: /note= "conserved core of fibronectin type
CC OTHER INFORMATION: III-like repeat"
CC FEATURE:
CC NAME/KEY: Domain
CC LOCATION: 707..760
CC OTHER INFORMATION: /label= FLR
CC OTHER INFORMATION: /note= "conserved core of fibronectin type
CC OTHER INFORMATION: III-like repeat"
CC FEATURE:
CC NAME/KEY: Domain
CC LOCATION: 809..857
CC OTHER INFORMATION: /label= FLR
CC OTHER INFORMATION: /note= "conserved core of fibronectin type
CC OTHER INFORMATION: III-like repeat"

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MIRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 27 16:03:06 1999; Maspar time 75.66 Seconds
1011.559 Million cell updates/sec
Tabular output not generated.

Title: >US-08-956-991-2
Description: (1-1910) from US08956991A.pap
Perfect Score: 1516
Sequence: 1 MWILALSLFOSFANVSEDL.....KALGVYTSYICLHLEMTFC 1910

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 57.625; Variance 121.630; scale 0.474

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	809	6.0	1028	2	I58164	BIG-1 protein - rat	3.78e-121
2	786	5.8	1028	2	A53449	plasmactoma-associat	9.58e-117
3	740	5.5	1447	2	A54100	tumor suppressor prot	5.75e-108
4	744	5.5	7962	2	I18346	elastic tctin - human	9.95e-109
5	720	5.3	1040	2	A49356	transient axonal glyco	3.65e-104
6	703	5.2	1036	2	S22383	axonin 1 precursor -	6.14e-101
7	701	5.2	1040	2	A34595	axonal glycoprotein T	1.47e-100
8	707	5.2	1427	2	I51669	tumor suppressor - Af	1.07e-101
9	680	5.0	1239	2	A43425	Bravo/Nr-CAM cell adh	1.39e-95
10	677	5.0	1268	2	A39640	neural cell adhesion	5.12e-96
11	663	4.9	1010	2	JU0094	fil protein precursor	2.25e-93
12	663	4.9	1091	2	S01998	contactin precursor -	2.25e-93
13	631	4.7	1018	2	A54744	contactin 1 precursor	2.36e-87
14	629	4.7	1018	2	I37246	contactin - human	5.60e-87
15	631	4.7	1020	2	S05944	neutonal cell surface	2.36e-87
16	631	4.7	1021	2	A57112	contactin precursor -	2.36e-87
17	637	4.7	1259	2	S36126	neural cell adhesion	1.76e-88
18	637	4.7	1260	2	S05479	neural cell adhesion	1.76e-88
19	640	4.7	1896	2	S46216	leukocyte antigen-rel	4.81e-89
20	620	4.6	1257	2	A41060	neural cell adhesion	2.73e-85
21	622	4.6	1894	2	C54689	protein-tyrosine-phos	1.15e-85
22	613	4.5	1018	2	JC4211	neural adhesion prote	5.59e-84
23	609	4.5	2029	1	TDFLTK	protein-tyrosine-phos	3.13e-83

RESULT ENTRY	1	ALIGNMENTS
TITLE	I58164	*type complete
ORGANISM	BIG-1 protein - rat	
DATE	26-Jul-1996	#formal_name Rattus norvegicus #common_name Norway rat
ACCESSION	I58164	26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Sep-1998
REFERENCE	I58164	
authors	Yoshihara, Y., Kawasaki, M., Tan, A., Tamada, A., Nagata, S., Kagamiyama, H., Morit, K.	
#journal	Neuron (1994) 13:415-426	
#title	BIG-1: a new TAG-1/F3-related member of the immunoglobulin superfamily with neurite outgrowth-promoting activity.	
#cross-references	MUID:94338697	
#accession	I58164	
##status	preliminary: translated from GR/EMBL/DBJ	
##molecule_type	mRNA	
##residues	1-1028	#label RES
##cross-references	EMBL:U11031; NID:9563132; PID:9563133	
GENETICS		
##gene	BIG-1	
CLASSIFICATION	#superfamily contactin; fibronectin type III repeat homology; Immunoglobulin homology	
SUMMARY	#length 1028 #molecular_weight 112788 #checksum 5866	
Query Match	6.0%; Score 809; DB 2; Length 1028;	
Best Local Similarity	24.7%; Pred. No. 3.78e-121;	
Matches	250; Conservative 249; Mismatches 447; Indels 66; Gaps 54;	

Db	25	GPVFKPE-SNSIPP-V-GSEDKITLNCARNPSPDHRRMQLNSGSDITSLDRK-L 79
Oy	306	GRLYKQPLKATISPRKYSVGSQVSLSCSVTGTEDQLSWNGCILNKGKVRITGI 365
Db	80	NGNLIIVINPRNMDTGSYOCFA-TNSIGTIVSREAKIOFAYLENFKSRMRSVAREQ 138
Oy	366	NHENLTIMHMKV-DGCAVYQCFVRKDKLSADQYOVVLEDC-TTKIISASEK-VSPA 422
Db	139	GVLLCGPPHSGELSVWVNEPSEFVEDSRFVSQETGHLIAKVPESVGNVTCV 198
Oy	423	PSVLMCNKVG-TPLPTITWILDDP-LKGSGR-ISO---M-ITS-E-GNVSYLNIS 472
Db	199	TSTVIMARVLSPTPLVLRSDGWMGEYPKIELOPETLPAAKG-STV-K---LECFAL 252
Oy	473	SSQVVDGGVY-RCTA-N-NSAGVY-LVQARINVRPAPSRPMKNTALAGADITIHQVI 528
Db	253	GNVPQJNMV-RRSDGMPPTK-IKLRFNGVLEIPNFQOE-DTSYEC-IAENSRGNVA 308

QY 529 GYPYYSIKWYKNSNLLPFRHROVAFEN-NGTLKLSDVOKVEDEGEYTCNVLVQPOLSTSQ 587

Db 309 RGRLLTYANRPYVOLLKDVETAVEDSLYWECPRA-SGKPPSPSTRMLKNGAL--VLEERIQ 365

QY 588 SVHATYVKVPPF-IQPFEPFRFSIGQRFVIPCIVVSGDLPIITITWQDKGRIPGSGLVITID 646

Db 366 -IE-NGALTIANLVNDSGFMQIAENKHGLIYSSAELVLVASAPFSSNPMMKIMOV 423

QY 647 NIDFTSSLRISNLIMHNGVYTCIARNEAAVEHOSOL-IVRPPKFFVQPP-RDODGI-Y 703

Db 424 GSVLIIDCKKSPRALSEFK--KGDYVVR-EQ-A--RISLNDGGLKIMNYTKADGI 476

QY 704 GKAVILNCSGEGRPVPTIYWKFSKAGVPOFQIALNGRIQVLSNGLIKHVEEDSGY 763

Db 477 YTCIAENQFGKANGTTO-LVTEPTRIILAPSNMDVAVGESIILPCOVQHDPLDIMFAM 535

QY 764 YLCKVSNVDGADYSKMYLTVKIPAMITSYPNITLATQOQKEMSCJAHGKPI-IV-RW 821

Db 536 YFNGTLIDFKKDGSHFE-K-VGSSSGDGLMIRNIOQLKHSKGYCMVOTGVDSSAAELI 593

QY 822 EKEDRIINPEMARIYVSTKEVGEVISTLOILPTVREDSGFESCHAINSDEGRGIIQLT 881

Db 594 VRGSPGPPEWVKYDEITDITLAQLSMTGDSHSPVSIYAVQARTPFSVGOMVRYTPEAI 653

QY 882 VOEPDPPPE-IEIKVYKAKITILRMWGFQDGNSPITGYDILCKNK-SDSWSAQRTKD-V 538

Db 654 DGTTRATVELNPMWYEFRRVYVASKIGGEPSSLSEKRTTEAPAEVAPSPVSGGGS 713

QY 939 SPOLNSATIIDHPSSTYSIRMYAKNRIGSEPS-NELITTADEAPADGPOCVHLEPIS 997

Db 714 RSELVITMDPVEELONGGFGFYVAFRPLGVTTWIO-TVVT-SPDNPRYFRNESTVVF 771

QY 998 SOSIRVYWKAPKHHLONGIIRGOYIGREYSTGNGFQFNISVDTSGDSEVYITLDNLNF 1057

Db 772 SPYEVKGVYNNKGEPSPVTVFSAEERTVAPSHISHSLSSEIEVSNMTITWKS 831

QY 1058 TOYGLVQACNAGTGPSSOEIITITLEDVPSYPPEVQAIATSPESISISWSTLSKEAL 1117

Db 832 NGRLIGEVRYWNNNGEESSSKVKVAGNOTSAVLRLGKSNLAYVAVRATYNTAGAPFS 891

QY 1118 NGILOGFRVIYWANLMDGELGEIKNITTTQPSLELDGLEYKTNYSIOVLAFTRAGDQVRS 1177

Db 892 ATVNATTKTTPSOPPGNVVWNAATDTKVLNMEQVKALENSEVYGVKVFRTSSQNNO 951

QY 1178 EOIFRTKEDVGPAGVKAASASWVFSW--LPPLKNGIIRKTYVFCSHPTVIS 1235

Db 952 VLNTNKTSAELLP-I-KE-DYIIEVKATTDGCGTSSQEIIRIPRITSMAR 1000

QY 1236 EFASPDSEFSYRIPNLRSNRQYSWVAVTSAGRNSSEIITVEPLAKAPAR 1287

RESULT 2

ENTRY A53449 #type complete

TITLE plasma cytoma-associated neuronal glycoprotein PANG - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 25-Aug-1999 #sequence_revision 25-Aug-1995 #text_change 18-Sep-1998

ACCESSIONS A53449

REFERENCE A53449

AUTHORS Connelly, M.A.; Grady, R.C.; Mushinski, J.F.; Marcu, K.B.

JOURNAL Pr. C. Natl. Acad. Sci. U.S.A. (1994) 91: 137-1341

TITLE PANG, a gene encoding a neuronal glycoprotein, is ectopically activated by intracisternal A-type particle long terminal repeats in murine plasmacytomas.

cross-references MUID:94151325

accession A53449

status preliminary

molecule_type mRNA

residues 1-1028 #label CON

cross-references GB:101991; NID:q200056; PID:q200057

classification #superfamily_contactin: fibronectin type III repeat homology; immunoglobulin homology

KEYWORDS glycoprotein

SUMMARY #length 1028 #molecular-weight 113151 #checksum 4174

Query Match 5.88; Score 786; DB 2; Length 1028;

Best Local Similarity 24.68; Pred. No. 9,58e-117;

Matches 249; Conservative 246; Mismatches 451; Indels 65; Gaps 54;

Db 25 GPVFEKEP-SNSIFP--VDSE-DKKTITLNCAGRNPSPHYRMOLNGSDIDTSLDHRK-L 79

QY 306 GRLLVQKPLKATISPRKVKSSVGSVSLSCSYGTGDOELSWRNELINPGKNVATIGI 365

Db 80 NGNLIIVINPNRNDGTSYOCFA-TNSLGTIVSREAKLOFAYLENFKTRMRSTVSYREQ 138

QY 366 NHEMLIDHWKVS-DGGAYOCFVAKDKLSADQVYVULEDG-TPKTIISAFSEKV-VSPA 422

Db 139 GVVLICGPPRHSGSLSYANVYNEPSPFVEEDSRISQDGHYLIKAVPESDVGNVTCV 198

QY 423 PVSLMCNVKG-TPLPTITWITIDDP-ILKGSIR-ISO---M-ITS-E-GNVYSILNIS 472

Db 199 TSTVNTFRVLGSPITPLVLRSDGVGEYEPKIEVOFPETLPAKG-STV--R--LECFAL 252

QY 473 SSOYRDSGVY-RCTA-N-NSAGVY-LVQARINVRGPASTIRPMKNITAIAGRDYIHCRAI 528

Db 253 GNPVPOIWM-RRSGMPPPNK-ILKRFNGMLEIQNFQDE-DTGSYE-GIAENSRKKNVA 308

QY 529 GYPYYSIKWYKNSNLLPFRHROVAFEN-NGTLKLSDVOKVEDEGEYTCNVLVQPOLSTSQ 587

Db 309 RGRLLTYANRPYVOLLKDVETAVEDSLYWECPRA-SGKPPSPSTRMLKNGAL--VLEERIQ 365

QY 588 SVHATYVKVPPF-IQPFEPFRFSIGQRFVIPCIVVSGDLPIITITWQDKGRIPGSGLVITID 646

Db 594 VRGSPGPPEWVKYDEITDITLAQLSMTGDSHSPVSIYAVQARTPFSVGOMVRYTPEAI 653

QY 882 VOEPDPPPE-IEIKVYKAKITILRMWGFQDGNSPITGYDILCKNK-SDSWSAQRTKD-V 538

Db 654 DGTTRATVELNPMWYEFRRVYVASKIGGEPSSLSEKRTTEAPAEVAPSPVSGGGS 713

QY 939 SPOLNSATIIDHPSSTYSIRMYAKNRIGSEPS-NELITTADEAPADGPOCVHLEPIS 997

Db 714 RSELVITMDPVEELONGGFGFYVAFRPLGVTTWIO-TVVT-SPDNPRYFRNESTVVF 771

QY 998 SOSIRVYWKAPKHHLONGIIRGOYIGREYSTGNGFQFNISVDTSGDSEVYITLDNLNF 1057

Db 772 SPYEVKGVYNNKGEPSPVTVFSAEERTVAPSHISHSLSSEIEVSNMTITWKS 831

QY 1058 TOYGLVQACNAGTGPSSOEIITITLEDVPSYPPEVQAIATSPESISISWSTLSKEAL 1117

Db 832 NGRLIGEVRYWNNNGEESSSKVKVAGNOTSAVLRLGKSNLAYVAVRATYNTAGAPFS 891

QY 1118 NGILOGFRVIYWANLMDGELGEIKNITTTQPSLELDGLEYKTNYSIOVLAFTRAGDQVRS 1177

Db 892 ATVNATTKTTPSOPPGNVVWNAATDTKVLNMEQVKALENSEVYGVKVFRTSSQNNO 951

QY 1178 EOIFRTKEDVGPAGVKAASASWVFSW--LPPLKNGIIRKTYVFCSHPTVIS 1235

Db 952 VLNTNKTSAELLP-I-KE-DYIIEVKATTDGCGTSSQEIIRIPRITSMAR 1000

QY 1236 EFASPDSEFSYRIPNLRSNRQYSWVAVTSAGRNSSEIITVEPLAKAPAR 1287

 WIRE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Jul 27 16:07:31 1999: Maspar time 52.29 Seconds
 1032.554 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-956-991-2
 Description: (1-1910) from US08956991A.pep
 Perfect Score: 13.15
 Sequence: 1 MMLALSLPQSFANFSEDL.....KAIGVTSYICLTLEWTF 1910

Scoring table: PAM 150
 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 58.685: Variance 101.910: scale 0.576

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	744	5.5	1447	1	DCC_MOUSE	TUMOR SUPPRESSOR PROTE	3.51e-132
2	740	5.5	1447	1	DCC_HUMAN	TUMOR SUPPRESSOR PROTE	2.94e-131
3	720	5.3	1040	1	AXOI_HUMAN	AXONIN-1 PRECURSOR (AX	1.21e-126
4	703	5.2	1036	1	AXOI_CHICK	AXONIN-1 PRECURSOR (AX	9.86e-123
5	701	5.2	1040	1	AXOI_RAT	AXONIN-1 PRECURSOR (AX	2.84e-122
6	677	5.0	1284	1	NRCA_CHICK	NG-CAM RELATED CELL AD	9.14e-117
7	663	4.9	1010	1	CONT_CHICK	CONTACTIN PRECURSOR (C	1.46e-113
8	631	4.7	1018	1	CONT_HUMAN	CONTACTIN PRECURSOR (C	2.92e-106
9	631	4.7	1020	1	CONT_MOUSE	CONTACTIN PRECURSOR (C	1.26e-107
10	637	4.7	1259	1	CAML_RAT	NEURAL CELL ADHESION M	1.26e-107
11	637	4.7	1260	1	CAML_MOUSE	NEURAL CELL ADHESION M	1.26e-107
12	620	4.6	1257	1	CAML_HUMAN	NEURAL CELL ADHESION M	9.27e-104
13	609	4.5	2029	1	LAR_DROME	PROTEIN-TYROSINE PHOSP	2.91e-101
14	598	4.4	1887	1	PTPF_HUMAN	LAR PROTEIN PRECURSOR	9.03e-99
15	570	4.2	837	1	NCM2_MOUSE	NEURAL CELL ADHESION M	1.90e-92
16	562	4.2	837	1	NCM2_HUMAN	NEURAL CELL ADHESION M	1.20e-90
17	562	4.2	1239	1	NRG_DROME	NEUROGLIAN PRECURSOR.	1.20e-90
18	574	4.2	1912	1	PTPD_HUMAN	PROTEIN-TYROSINE PHOSP	2.38e-93
19	558	4.1	1091	1	NCAL_CHICK	NEURAL CELL ADHESION M	9.48e-86
20	543	4.0	848	1	NCAL_HUMAN	NEURAL CELL ADHESION M	2.19e-86
21	524	3.9	1088	1	NCAL_XENLA	NEURAL CELL ADHESION M	3.87e-82
22	523	3.9	1092	1	NCAL_XENLA	NEURAL CELL ADHESION M	6.46e-82
23	531	3.9	1266	1	NGCA_CHICK	NEURONAL GLIAL CELL AD	1.06e-83

24	509	3.8	761	1	NCAL_HUMAN	NEURAL CELL ADHESION M	8.45e-79
25	498	3.7	853	1	NCAL_BOVIN	NEURAL CELL ADHESION P	2.33e-76
26	496	3.7	1115	1	NCAL_MOUSE	NEURAL CELL ADHESION M	6.47e-76
27	492	3.6	858	1	NCAL_RAT	NEURAL CELL ADHESION P	4.97e-75
28	476	3.5	725	1	NCAL_MOUSE	NEURAL CELL ADHESION M	6.14e-72
29	401	3.0	898	1	PAS2_SCHAM	FASCICLIN II PRECURSOR	3.59e-55
30	402	3.0	3707	1	PGM_MOUSE	BASEMENT MEMBRANE-SPC	2.19e-55
31	378	2.8	811	1	FS22_DROME	FASCICLIN II, PHOSPHAT	2.95e-50
32	378	2.8	873	1	FS21_DROME	FASCICLIN II, MEMBRANE	2.95e-50
33	364	2.7	4393	1	PGBL_HUMAN	BASEMENT MEMBRANE-SPC	2.73e-47
34	313	2.3	2477	1	FINC_RAT	FIBRONECTIN PRECURSOR	1.13e-36
35	308	2.3	2477	1	FINC_MOUSE	FIBRONECTIN PRECURSOR	1.13e-36
36	313	2.3	2481	1	UN52_CAEEL	BASEMENT MEMBRANE PROT	1.13e-36
37	294	2.2	2265	1	FINC_BOVIN	FIBRONECTIN (FN).	8.32e-33
38	287	2.1	345	1	OPCM_BOVIN	OPLOID BINDING PROTEIN	2.14e-31
39	284	2.1	345	1	OPCM_HUMAN	OPLOID BINDING PROTEIN	8.55e-31
40	279	2.1	345	1	OPCM_RAT	OPLOID BINDING PROTEIN	8.54e-30
41	286	2.1	1131	1	CPSE_CHICK	C-PROTEIN, SKELETAL MU	3.40e-31
42	262	1.9	333	1	AMAL_DROME	AMALGAM PROTEIN PRECUR	1.97e-26
43	255	1.9	353	1	CEPU_CHICK	CEPU-1 PROTEIN PRECURS	4.60e-25
44	257	1.9	1328	1	FINC_PLENA	FIBRONECTIN (FN) (FRAG	1.87e-25
45	262	1.9	2386	1	FINC_HUMAN	FIBRONECTIN PRECURSOR	1.97e-26

ALIGNMENTS

RESULT 1
 ID DCC_MOUSE STANDARD: PRT: 1447 AA.

AC P02111;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.

OS MUS MUSCULUS (MOUSE).

OC EURKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC RODENTIA; SCIROGNATHI; MORIDAE; MORINAE; MUS.

OC [1]

RC STRAIN-BALB/C; TISSUE-BRAIN;

RC MEDLINE: 96112625.

RA COOPER H.M., ARMES P., BRITTO J., GAD J., WILKS A.F.;

RT "Cloning of the mouse homologue of the deleted in colorectal cancer

gene (mdcc) and its expression in the developing mouse embryo.";

RL ONCOGENE 11:2243-2254(1995).

RL [2]

RP REVISIONS.

RC STRAIN-BALB/C; TISSUE-BRAIN;

RA COOPER H.M.;

RL SUBMITTED (JUN-1995) TO EMBL/GENBANK/UDJ DATA BANKS.

CC -1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE

DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN

BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.

CC -1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS

EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION

AND REMAIN AT THIS LEVEL IN THE ADULT.

CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM

THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD

FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY

ALTERNATIVE SPLICING.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

4 C2-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.

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the European Bioinformatics Institute. There are no restrictions on its

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or send an email to license@isb-sib.ch).

CC

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CC -----
DR EMBL: X85788; E264593; -.
DR MGD: MGI:94869; DCC.
DR PFM: PFM0041; fn3: 6.
DR PFM: PFM0047; 1g: 4.
DR HSP: P56276; 1TK.
KM GLYCOPROTEIN: IMMUNOGLOBULIN FOLD: TRANSMEMBRANE: SIGNAL:
AMT-ONCOGENE: ALTERNATIVE INITIATION: ALTERNATIVE SPLICING.
FT SIGNAL 1 25
FT CHAIN 26 1447
FT CHAIN 85 1447
FT CHAIN 26 1097
FT DOMAIN 1098 1122
FT TRANSFM 1123 1447
FT DOMAIN 1123 1447
FT DOMAIN 54 124
FT DOMAIN 154 219
FT DOMAIN 254 317
FT DOMAIN 345 407
FT DOMAIN 426 522
FT DOMAIN 525 618
FT DOMAIN 619 716
FT DOMAIN 722 816
FT DOMAIN 840 940
FT DOMAIN 941 1042
FT DISULFID 61 117
FT DISULFID 161 212
FT DISULFID 261 310
FT DISULFID 352 400
FT CARBOHYD 60 60
FT CARBOHYD 94 94
FT CARBOHYD 299 299
FT CARBOHYD 318 318
FT CARBOHYD 478 478
FT CARBOHYD 628 628
FT CARBOHYD 702 702
FT VARSPIC 819 838
FT SEQUENCE 1447 AA; 158298 MW; F5FB79BA CRC32;

Query Match 5.5%; Score 744; DB 1; Length 1447;
Best Local Similarity 29.6%; Pred. No. 3,51e-132;
Matches 228; Conservative 178; Mismatches 293; Indels 72; Gaps 55;

Db 72 IWKKDGILALGMDRKQQLPENGSLILNLSHRHMRDEGLYCENSLADSSJISRT 131
OY IWKYKNS-NL-LPFNHRQVAFENNGLT-K-LSDVQKVEDEGEYICNV-LVQPOLSTSQS 588
Db 132 AVYTVAGLPRLSOTESIAP-MGDTVLKCEVIGEPMP-TIHMKNOODL-NPLPGSR 188
OY VHYTVAVP-PFTQPE-PFESIGORVFLPCVAVSGDLPIITWOKDGRPIPGSLGVITD 646
Db 189 VVVLPSGALQISRLPGDGVYRCSARNPASIRTSNEAEVRLSLPGHLKOLYFLQRPSPN 248
OY NIDFTS-SLRISLSLHMGNYTCIARNEAA-VEHQSOL-IVRVP-PK-FVVG-PRD 698
Db 249 VIAIEKDNVLECCVSGYPPPSFTW-L-RGEVYDLR--S-K-KSLGLGSLLSNWT 302
OY OOGIYKAVILNCSAGYEVPTIWMKFSKAGVPOFOPIALNGRIQVLSNGSTLKHAVE 758
Db 303 DSGITCVVTK-NENISASAEILTVLPWFLNHPNLSYAESMDIEPECVSG-KVVP 360
OY EDSGYLLCKVSNVDGADVSKSMITIKITAMITSTPNTLT.TOGQKKEKSTAHGFKPI- 817
Db 361 TVNMKNKGVDVIP-S-D-YF-QI--VGG---SNLRILGVK DEGEYQCAENAGNAOSS 412
OY IYWEKEDRILNEMARVLYSTIKVEGEVISTQILPTLRSDSGFFSCHAINSYGEDRGI 877
Db 413 AOLIVKPAIPSSILPSAPROVLPVLSRVRSLMRPAKKNIOITVFFSREDN 472
OY IOLTVQEPDPPE-I--ET-KDV-----KARITILRMWGMFGNSPITIGYDECKNKKDS 928
Db 473 REBALNTTQPGS-IQ-LYGNLKPAMATYFRVAAYENMGCESSPIKATOPDELQVGP 530
OY WDSAQNTKTVSPOLNSATIIIDHPSSTYSIRMAKNRICKSEPSNELLITAD-ENAPDGP 987

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Db 531 VENLHAVSTPSILITWPPA-Y-ANGPVQRYLCEVSTGKE-Q-NI-EVD--GLS- 582
OY POEVHLEPISOSIRVTKWAPKKHLONGIIRGQIGREYSTGCFNFINISVDTSCDS 1047
Db 583 -YKLEGLAKFTEYTLFLFVANNVGVSTDDITVLTSLDVPAPPNISLSEVNSRSIKV 641
OY 1048 VYTLDMNLNFTQGLVVOACNCRAGTSPSSQSEIITTLDEVPYPPENVOALATSPESISI 1107
Db 642 SMLPPSGTONGITGKIRHRRKTRRGEM-ETLE-PNNLWL-PTGLEKSGSYSFQVSA 698
OY 1108 SWSLTSKEALNGLGCFRITYANLMDGELGKIKTTTQPSLEDGLEKTYNTSIQVLA 1167
Db 699 MTVNGTGPSPSNWYTAETPENDLDESQVDPDPSLHVRFQNCII-MSWTPLNPIVVG 757
OY 1168 FTRAGGVASE-QIFTRKE-D---VPGPAGVAKAAASASMVSWMLPLKLNGIRK 1221
Db 758 YITIGYGVSPYAEYTRV-DSK-QRY-YSTIERLESSHYVLSIKAPNNMGEG 805
OY 1222 YTV-F-CshpYPTVISEFASPSFSYRIPNLRRROYSWVAVTSAGRG 1270

RESULT 2
ID DCC_HUMAN STANDARD; PRT: 1447 AA.
AC P43146;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).
GN DCC.
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95011532
RA HEDRICK L., CHO K.R., FEARON E.R., WU T.-C., KINZLER K.W.,
RT "The DCC gene product is cellular differentiation and colorectal
RT tumorigenesis."
RL GENES DEV. 8:1174-1183(1994).
RN [2]
RP SEQUENCE OF 1-750 FROM N.A.
RX MEDLINE: 90100559.
RA FEARON E.R., CHO K.R., NIGRO J.M., KERN S.E., SIMONS J.W.,
RA RUPPERT J.M., HAMILTON S.R., PREISINGER A.C., THOMAS G., KINZLER K.W.,
RA VOGELSTEIN B.:
RT "Identification of a chromosome 18q gene that is altered in
RT colorectal cancers."
RL SCIENCE 247:44-56(1990).
RN [3]
RP SEQUENCE OF 107-472 FROM N.A. (SCRAMBELD EXONS).
RX MEDLINE: 91121517.
RA NIGRO J.M., CHO K.R., FEARON E.R., KERN S.E., RUPPERT J.M.,
RA OLINER J.D., KINZLER K.W., VOGELSTEIN B.:
RT "Scrambled exons."
RL CELL 64:607-613(1991).
RN [4]
RP GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.
RX MEDLINE: 94245241.
RA CHO K.R., OLINER J.D., SIMONS J.W., HEDRICK L., FEARON E.R.,
RA PREISINGER A.C., HEDGE P., SILVERMAN G.A., VOGELSTEIN B.:
RT "The DCC gene: structural analysis and mutations in colorectal
RT carcinomas."
RL GENOMICS 19:525-531(1994).
RN [5]
RP VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.
RX MEDLINE: 94243823.
RA MIYAKE S., NAGAI K., YOSHINO K., OTO M., ENDO M., YUASA Y.:
RT "Point mutations and allelic deletion of tumor suppressor gene DCC in
RT human esophageal squamous cell carcinomas and their relation to
RT metastasis."
RL CANCER RES. 54:3007-3010(1994).

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 27 16:11:31 1999; Maspar time 107.09 Seconds

Tabular output not generated. 973.465 Million cell updates/sec

Title: >US-08-956-991-2

Description: (1-1910) from US08956991A.pep

Perfect Score: 13516

Sequence: 1 MMLALSLFQSFANVFSEDL.....} IGVVSYICLHLEKTCFC 1910

Scoring table: PAM 150

Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl9
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 56.959; Variance 104.912; scale 0.543

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	DB	ID	Description	Pred. No.
1	13406	99.2	896	4	060468	DOWN SYNDROME CELL ADH	0.00e+00
2	11119	82.3	1571	4	060469	DOWN SYNDROME CELL ADH	0.00e+00
3	809	6.0	1028	11	062682	BIG-1 PROTEIN PRECURSO	1.99e-139
4	785	5.8	1028	11	007409	PLASMACYTOMA-ASSOCIATE	2.23e-134
5	741	5.5	1445	11	063155	COLORECTAL TUMOR SUPP	1.57e-124
6	744	5.5	7962	4	010465	TITIN, SKELETAL MUSCLE	3.47e-125
7	734	5.4	1099	11	P97527	NB-2.	5.28e-123
8	707	5.2	1427	13	091562	TUMOR SUPPRESSOR.	4.01e-117
9	695	5.1	1026	11	062845	NEURAL CELL ADHESION P	1.62e-114
10	689	5.1	1277	13	098902	NEURAL CELL ADHESION M	3.26e-113
11	696	5.1	1377	11	P97603	NEOGENIN (FRAGMENT).	9.86e-115
12	694	5.1	1395	5	044824	ROUNDABOUT 1.	2.68e-114
13	692	5.1	4162	13	098818	CONNECTIN/TITIN (FRAGM	7.28e-114
14	674	5.0	1224	4	000533	NEURAL CELL ADHESION M	5.82e-110
15	667	4.9	1005	13	P79921	CONTACTIN/F3/F11.	1.91e-108
16	668	4.9	1009	13	093250	CONTACTIN A.	1.16e-108
17	647	4.8	1612	11	089026	DUT11 PROTEIN.	3.99e-104
18	644	4.8	15198	5	075518	HEMICENTIN PRECURSOR.	1.77e-103
19	630	4.7	1021	11	063198	RAT NEURAL ADHESION MO	1.84e-100
20	638	4.7	1461	4	000340	NEOGENIN.	3.48e-102

21	634	4.7	1461	4	Q92859	NEOGENIN.	2.53e-101
22	629	4.7	1651	11	O55005	TRANSMEMBRANE RECEPTOR	3.02e-100
23	640	4.7	1898	11	O64604	LEUCOCYTE COMMON ANTIG	1.29e-102
24	627	4.6	1180	4	O15051	KIAA0343.	8.14e-100
25	617	4.6	1197	13	Q90478	ADHESION MOLECULE L1.1	1.15e-97
26	620	4.6	5197	5	O10036	HYPOTHETICAL 571.5 KD	2.60e-98
27	613	4.5	1018	6	Q28106	F3/F11/CONTACTIN PREC	8.30e-97
28	612	4.5	1264	5	P91767	NEUROGLIAN.	1.36e-96
29	583	4.4	1028	11	P97528	NB-3.	1.88e-91
30	588	4.4	1299	4	O15179	NRCAM PROTEIN.	1.88e-91
31	578	4.3	1209	13	P70232	CLOSE HOMOLOGUE OF L1	2.57e-89
32	580	4.3	1277	13	Q90284	L1-LIKE CELL ADHESION	9.62e-90
33	587	4.3	1323	13	Q08476	CONNECTIN (TITIN) (FRA	3.08e-91
34	567	4.2	1215	11	P97685	NG-CAM RELATED CELL AD	5.69e-87
35	566	4.2	1904	11	Q64699	PROTEIN TYROSINE PHOSP	9.29e-87
36	570	4.2	1907	11	Q64503	PROTEIN TYROSINE PHOSP	1.31e-87
37	568	4.2	1911	1	O15718	PPRSGMA PRECURSOR (EC	3.48e-87
38	550	4.1	1239	5	O61541	NEUROGLIAN.	2.34e-83
39	550	4.1	1302	5	O61542	NEUROGLIAN.	2.34e-83
40	539	4.0	846	13	O57577	NCAM-140.	5.03e-81
41	539	4.0	1100	13	O57576	NCAM-180.	5.03e-81
42	545	4.0	1493	11	P97798	NEOGENIN (NEOGENIN PRO	2.69e-82
43	527	3.9	1070	4	O13417	TRANSMEMBRANE RECEPTOR	1.74e-78
44	532	3.9	1299	4	Q92823	HERANO/NR-CAM PRECURSO	1.52e-79
45	530	3.9	1415	5	Q94155	UNC-40 (11984.6 PROTEI	4.03e-79

ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	1896 AA.
AC	060468				
DT	01-AUG-1998 (TREMBLREL. 07, CREATED)				
DT	01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)				
DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)				
DE	DOWN SYNDROME CELL ADHESION MOLECULE (FRAGMENT).				
GN	DSICAM.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;				
OC	CATARRHINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN.				
RA	YAMAKAWA K., HUO Y.-K., HAENDEL M.A., HUBERT R., CHEN X.-N.,				
RA	LYONS G.E., KORENBERG J.R.;				
RL	SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.				
DR	EMBL: AF023449; G3169766; ..				
FT	NON_TER	1	1		
SO	SEQUENCE	1896 AA;	209745 MW;	ODE6UCCE CRC32;	

Query Match 99.24; Score 13406; DB 4; Length 1896;
Best Local Similarity 100.0%; P-Val. No. 0.00e+00;
Matches 1896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	VFSEDLHSLYFNVASLOEVFASTTGLVPCPACGIPVTLKMYLATGEIYDVGRH	60
Qy	15	VFSEDLHSLYFNVASLOEVFASTTGLVPCPACGIPVTLKMYLATGEIYDVGRH	74
Db	61	VHPNGTLOIFPPSPSTLTHDNTTYCTAENPSGKIRSDVHIKAVLRPYTVREDDK	120
Qy	75	VHPNGTLOIFPPSPSTLTHDNTTYCTAENPSGKIRSDVHIKAVLRPYTVREDDK	134
Db	121	TMRGVAVFKCIIPSSVEAYITVSWEKDVSLVSGSRFLITSGALYIKDVONEDGLN	180
Qy	135	TMRGVAVFKCIIPSSVEAYITVSWEKDVSLVSGSRFLITSGALYIKDVONEDGLN	194
Db	181	YRCITRRHYTGETQSSARLPVSDPANSAPIIDGDRKKAAGQVLPKCALGHP	240
Qy	195	YRCITRRHYTGETQSSARLPVSDPANSAPIIDGDRKKAAGQVLPKCALGHP	254
Db	241	DYRLKDNMPLELSGRQKVTGTLINIRPSDGSVYCEVSNRYGTAKYIGRLYKQPL	300
Qy	255	DYRLKDNMPLELSGRQKVTGTLINIRPSDGSVYCEVSNRYGTAKYIGRLYKQPL	314

D	b	301	KATISPRKXKSSVGSQVSLSCSYGTGEDQELSMWRKNEILLPCKXNRITGINHEMLIMDH	360
O	y	315	KATISPRKXKSSVGSQVSLSCSYGTGEDQELSMWRNEILLPCKXNRITGINHEMLIMDH	374
D	b	361	MWSDGAVQCEVRKDKLSADBYVOVVLJEDTQPKLISAFSEKVVSPAEPVSLMCNVKGP	420
O	y	375	MWSDGAVQCEVRKDKLSADBYVOVVLJEDTQPKLISAFSEKVVSPAEPVSLMCNVKGP	434
D	b	421	LPRTITWLDDDPILKGGSHRISQMITSEGNVSTLNLSSQVRDGYRYRCTANNSAGYL	480
O	y	435	LPRTITWLDDDPILKGGSHRISQMITSEGNVSTLNLSSQVRDGYRYRCTANNSAGYL	494
D	b	481	YQARIWVRGPASIRPKKNTITALAGDQTYIHCVRGIVGPYYSIKWKXNSNLJPFHNRQVAF	540
O	y	495	YQARIWVRGPASIRPKKNTITALAGDQTYIHCVRGIVGPYYSIKWKXNSNLJPFHNRQVAF	554
D	b	541	NGTGLKLSVDQKVEDEGEYTCNVLVQPOLSTSQSVHYTKVPPFIQPEFPFSSIGORVF	600
O	y	555	NGTGLKLSVDQKVEDEGEYTCNVLVQPOLSTSQSVHYTKVPPFIQPEFPFSSIGORVF	614
D	b	601	IPCWVSGDLPIITTXQXKGRPIPSLGVTIDNIDFTSLISNLSLMHNGNTTCIARNE	660
O	y	615	IPCWVSGDLPIITTXQXKGRPIPSLGVTIDNIDFTSLISNLSLMHNGNTTCIARNE	674
D	b	661	AAAEHOSOLIVRVPKRVVQPPDOQGIYKAVAILNCSAEGYPVPIYWKFSKAGVPOF	720
O	y	675	AAAEHOSOLIVRVPKRVVQPPDOQGIYKAVAILNCSAEGYPVPIYWKFSKAGVPOF	734
D	b	721	QPIALNGRIOVLSNGSLLIKHYEEDSGYLLCKVSNDDVAGVSKSMYLTKYIPAMLTSPY	780
O	y	735	QPIALNGRIOVLSNGSLLIKHYEEDSGYLLCKVSNDDVAGVSKSMYLTKYIPAMLTSPY	794
D	b	781	NTTLATQOKKXKSCSTAHGKXPIIYWEKEDRIINPEMARLYVSTRKEVEEVISTDILP	840
O	y	795	NTTLATQOKKXKSCSTAHGKXPIIYWEKEDRIINPEMARLYVSTRKEVEEVISTDILP	854
D	b	841	TVREDSGFFSCHALINSYGEDRGILLOLTVOEPPDPPELIEKDYKARTTLRLMTWCFDQNSP	900
O	y	855	TVREDSGFFSCHALINSYGEDRGILLOLTVOEPPDPPELIEKDYKARTTLRLMTWCFDQNSP	914
D	b	901	ITGVDIIECKNKSDBSQAORTXQVSPQLMSATIIDIHPSSTYSIMYAKNRIGSEPSNE	960
O	y	915	ITGVDIIECKNKSDBSQAORTXQVSPQLMSATIIDIHPSSTYSIMYAKNRIGSEPSNE	974
D	b	961	LITITADEAPRGPQOEHLLEPISSOSIRYTWKAPKKHLLONGILRGYOLIGREYSTGQNFQ	1020
O	y	975	LITITADEAPRGPQOEHLLEPISSOSIRYTWKAPKKHLLONGILRGYOLIGREYSTGQNFQ	1034
D	b	1021	FNIISVDTSQSEYVITLDNLKFTQYGLVYQACNRAKGTQPSQOEIITTLLEDDVSYPEN	1080
O	y	1035	FNIISVDTSQSEYVITLDNLKFTQYGLVYQACNRAKGTQPSQOEIITTLLEDDVSYPEN	1094
D	b	1081	VOAINTSPESISISMSTLSEKALNGILOGFRVITYMANLMDGELGELIKNTTTOPSLELDG	1140
O	y	1095	VOAINTSPESISISMSTLSEKALNGILOGFRVITYMANLMDGELGELIKNTTTOPSLELDG	1154
D	b	1141	LEKTYNYSIOVLAFTRAGDVRSEQIFTRTKEDVPCRPAGCVKAAASASNFVSNLPLK	1200
O	y	1155	LEKTYNYSIOVLAFTRAGDVRSEQIFTRTKEDVPCRPAGCVKAAASASNFVSNLPLK	1214
D	b	1201	LNGLIIRKTYVCSHYPVIVISSEFASPDSTSYRPLNLSRNQYSWVYAVTISAGGNSSE	1260
O	y	1215	LNGLIIRKTYVCSHYPVIVISSEFASPDSTSYRPLNLSRNQYSWVYAVTISAGGNSSE	1274
D	b	1261	IITVEPLAKAPARILITFSGVITTEPMKMDIYLPCKAVGDPSPAYKMKMDSNGTSLVTIDG	1320
O	y	1275	IITVEPLAKAPARILITFSGVITTEPMKMDIYLPCKAVGDPSPAYKMKMDSNGTSLVTIDG	1334
D	b	1321	RMSITPSNGSFITRYVKAEDSGYVSCIANNNKNGSEIILNLQVONVPPDOPLRITVSTTSS	1380
O	y	1335	RMSITPSNGSFITRYVKAEDSGYVSCIANNNKNGSEIILNLQVONVPPDOPLRITVSTTSS	1394

Db	1381	TTLSWLPDNGGSSINGCYLLILOYSDENSDSEMGSPSPISRSRSTRLEMLNKGIMYKFTLLAQ	1440
Qy	1395	ITLSWLPDNGGSSINGCYLLILOYSDENSDSEMGSPSPISRSRSTRLEMLNKGIMYKFTLLAQ	1454
Db	1441	NGVOPGRISEIEKTKLTGKPGQSKCOELFASINTTRVRLNLIGNMDGCGPTTSETLEYR	1500
Qy	1445	NGVOPGRISEIEKTKLTGKPGQSKCOELFASINTTRVRLNLIGNMDGCGPTTSETLEYR	1514
Db	1501	PFGTWTTAQTORTSLSKSYLLIYDLOEATWYELOMRVCSAGCAEKOANPATLNTYGGSTIP	1560
Qy	1515	PFGTWTTAQTORTSLSKSYLLIYDLOEATWYELOMRVCSAGCAEKOANPATLNTYGGSTIP	1574
Db	1561	PLISVYQNEBGLTNTGLKMLVTISCTIIVGVLLFVLLLVYRRRRREROLKRLRDASKL	1620
Qy	1575	PLISVYQNEBGLTNTGLKMLVTISCTIIVGVLLFVLLLVYRRRRREROLKRLRDASKL	1634
Db	1621	AEMMSKTRISDPLSKOQOTFLRMHIDIPRAQLLIEERDTMETIIDRSYVLLTDADFGCA	1680
Qy	1635	AEMMSKTRISDPLSKOQOTFLRMHIDIPRAQLLIEERDTMETIIDRSYVLLTDADFGCA	1694
Db	1681	AKOKSLTATHTVHYOSVQATGPLVDYSDARPGTNPTRRNAAGCTARRARRASQWTLNR	1740
Qy	1695	AKOKSLTATHTVHYOSVQATGPLVDYSDARPGTNPTRRNAAGCTARRARRASQWTLNR	1754
Db	1741	PHPTISATTLTDMRLPAPRAAGVDKESDYSYSPSPQDTRARSSWVSTESASTYEEL	1800
Qy	1755	PHPTISATTLTDMRLPAPRAAGVDKESDYSYSPSPQDTRARSSWVSTESASTYEEL	1814
Db	1801	ARAYEHAKMEBOLRAKFTTIECFISDTSSEQLAGTNEYDLSJTSIPSESGICFTAS	1860
Qy	1815	ARAYEHAKMEBOLRAKFTTIECFISDTSSEQLAGTNEYDLSJTSIPSESGICFTAS	1874
Db	1861	PKPKDDGGRRVMMAPRAIGOVTSYICLHTEWFC	1896
Qy	1875	PKPKDDGGRRVMMAPRAIGOVTSYICLHTEWFC	1910
RESULT 2			
ID	060469	PRELIMINARY:	PRT: 1571 AA.
AC	060469:		
DT	01-AUG-1998 (TREMBREL. 07, CREATED)		
DT	01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATED)		
DT	01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)		
DE	DOWN SYNDROME CELL ADHESION MOLECULE.		
GN	DSCHM.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;		
OC	CATARRHINI; HOMINIDAE; HOMO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN:		
RA	YAMAANA K., HUO Y.-K., HANDEL M.A., HUBERT R., CHEN X.-N.,		
RA	LYONS G.E., KORENBERG J.K.,		
RL	SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.		
RL	EMBL: AF023450; G3169768; -		
SQ	SEQUENCE 1571 AA: 173803 MM; 5F8C77D1 CRC32:		
Query Match 82.3%: Score 1119: DB 4: Length 1571:			
Best Local Similarity 99.9%: Pred. No. 0.00e+00:			
Matches 1561: Conservative 1; Mismatches 0; Indels 0; Gaps 0			
Db	1	MMIALSLFOSFANVSEDLHSLSLFYVNASLDEVFASTGTGLVCPAPAGIPVTLRWYL	60
Qy	1	MMIALSLFOSFANVSEDLHSLSLFYVNASLDEVFASTGTGLVCPAPAGIPVTLRWYL	60
Db	61	ATGEELVDPGIRHVPNCTLOIFPPSSFSSTLHDNTYCTAENPSGKIRSDVHIKA	120
Qy	61	ATGEELVDPGIRHVPNCTLOIFPPSSFSSTLHDNTYCTAENPSGKIRSDVHIKA	120
Db	121	VLEPPTVAREDDKTRGNVAVFKCIPSSVAYITIVVSWEDOTSLVSGSRFLITISGA	180
Qy	121	VLEPPTVAREDDKTRGNVAVFKCIPSSVAYITIVVSWEDOTSLVSGSRFLITISGA	180

Query Match	82.3%	Score 11119	DB 4	Length 1571
Best Local Similarity	99.9%	Pred. No. 0.00e+00		
Matches 1561; Conservative	1	Mismatches 0	Indels 0	Gaps 0

Db	1	MMIALSLRQSFANVNSSEDLHLSLSLTFVNAVSLQEVFASTGTGLVPCPAAGIIPVTLIRVYL	60
Oy	1	MMIALSLRQSFANVNSSEDLHLSLSLTFVNAVSLQEVFASTGTGLVPCPAAGIIPVTLIRVYL	60
Db	61	ATGEELIYDVGIRHVRHNPNTLQIEPRPSSFTLLHDNNTYCTAEANPGKIRSOVNH1KA	120
Oy	61	ATGEELIYDVGIRHVRHNPNTLQIEPRPSSFTLLHDNNTYCTAEANPGKIRSOVNH1KA	120
Db	121	VLRPEYTVRVEDOKTRMGNAVAFKCIIPSSVZAYITVWSMEDVYSLVSGSFFLITSGA	180
Oy	121	VLRPEYTVRVEDOKTRMGNAVAFKCIIPSSVZAYITVWSMEDVYSLVSGSFFLITSGA	180